

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2000, 20:18:59 ; Search time 67.51 Seconds
(without alignments)
444.374 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQTATSPDGGTTFEHLWS.....PDCXARKQPIKEFTAEIHF 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR-62:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	851.5	25.2	396	1 JH0631	cellular tumor ant
2	778	23.0	367	1 S02193	cellular tumor ant
3	760.5	22.5	386	1 S1648	cellular tumor ant
4	749	22.1	396	1 JH0633	cellular tumor ant
5	741.5	21.9	393	2 JG6176	tumor suppressor p
6	741	21.9	363	1 A29376	cellular tumor ant
7	735.5	21.7	391	1 S02192	cellular tumor ant
8	724.5	21.4	391	2 JG6193	tumor suppressor p
9	724.5	21.4	393	1 DNH53	cellular tumor ant
10	718.5	21.2	393	1 S06594	cellular tumor ant
11	711.5	21.0	390	1 DNH53	cellular tumor ant
12	702	20.7	381	2 S38824	cellular tumor ant
13	248.5	7.3	77	2 I46226	p3 - dog (fragmen
14	151.5	4.5	903	2 T00074	hypothetical prote
15	145	4.3	864	2 T04518	hypothetical prote
16	139.5	4.1	1221	2 T13283	probable transcrip
17	133	3.9	1273	2 S58782	SFC31 protein - ye
18	131.5	3.9	2364	2 A56577	microtubule-associ
19	129	3.8	306	2 A4354	extensin precursor
20	127.5	3.8	784	2 S26638	SPR-1 protein - hu
21	126	3.7	817	2 S1342	verprolin - yeast
22	126	3.7	1791	2 T02909	hypothetical prote
23	125.5	3.7	1560	2 T02885	peroxisome prolif
24	125	3.7	1081	2 T13231	dachshund protein
25	124.5	3.7	2397	1 A55335	vesican precursor
26	124	3.7	650	2 T0487	hypothetical prote
27	124	3.7	1051	1 JW0051	serine/threonine-s
28	124	3.7	1099	2 A56155	tumor suppressor p
29	123.5	3.6	1618	2 S21424	nestin - human
30	123	3.6	1065	2 T13230	dachshund isoform

31	123	3.6	1638	2 A42091	transcription acti
32	123	3.6	2440	2 S39162	CREB-binding prote
33	123	3.6	2441	2 S39161	CREB-binding prote
34	123	3.6	2715	2 T13049	eyelid - fruit fly
35	122.5	3.6	1072	2 T13228	dachshund protein
36	122.5	3.6	1072	2 T13232	dachshund protein
37	122	3.6	1074	2 T13229	dachshund protein
38	122	3.6	1396	2 A44453	translation initia
39	118.5	3.5	635	1 WBEW6	capsid protein - h
40	118.5	3.5	968	2 S46932	protein p130 - rat
41	118.5	3.5	4957	2 T03455	ALR protein - huma
42	118.5	3.5	5262	2 T03454	ALR protein - huma
43	118	3.5	1081	2 S66736	transcription acti
44	118	3.5	1736	2 A47747	tight junction pro
45	116	3.4	620	2 S06733	hydroxyproline-ric

ALIGNMENTS

RESULT 1

JH0631

cellular tumor antigen p53 - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 10-Sep-1989 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0631

R:de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.

Gene 112, 241-245, 1992

A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.

A:Reference number: JH0631; MUID:92210006

A:Accession: JH0631

A:Molecule type: mRNA

A:Residues: 1-396 <DEF>

A:Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829

A:Experimental source: liver

C:Comment: This protein is the product of a tumor suppressor gene, p53, whose ir

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus

F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 25.2% Score 851.5; DB 1; Length 396;

Best Local Similarity 55.6%; Pred. No. 4.9e-52;

Matches 170; Conservative 43; Mismatches 86; Indels 7; Gaps 5;

QY 93 VPTHSPYAQPS-STFDIMS-PAPVPSNTDYPGPHFEVTFQSSSTAKSATWYSPLLKK 150

DB 61 VSATEPAPQPSISTDTGSPPTSTVPTSDPGALGFLRFLQSSSTAKSVTCTYSPDLNK 120

QY 151 LYCQAKTCPTQIKVSPPPPGTAIRAMPVYKKAHVTDVVKPCPNHGLRDFNEQSAP 210

DB 121 LFCQLAKTCPTQIVVDHPPPGAVRALATYKLLSDVADVRCRPHQSTSENEG-PAP 179

QY 211 ASHLIRVGNLSDYDPTVGRSVVYPPQVGTFTTILYFMCNSSCVGGMNRRP 270

DB 180 RGHVVRVGNORSEYMEDGNTLRHSVLVYPPQVSECTVLYFMCNSSCMGGMNRRP 239

QY 271 ILIITLMDRGVLRGRSREGRICACGDRKADHDHYEQALN-ESSAKNGAASKRA 329

DB 240 ILIITLMDRGVLRGRSREGRICACGDRKADHDHYEQALN-ESSAKNGAASKRA 299

QY 330 FKQSPVAPVAGVKKRRH---GDETTYLVQVRGNEFELMKLESLELMELVPOPLV 386

DB 300 MKEASLPAPQPGASKTKSSPAVSDDEIYTLQIRGEKYEMLKKFNDSLELSLPVADA 359

QY 387 DSYRQQ 392

DB 360 DKYRQK 365

RESULT 2

S02193

cellular tumor antigen p53 - chicken
N:Alternate names: nuclear oncoprotein p53
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02193
R:Soussi, T.; Beque, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A:Reference number: S02193; MUID:89083584
A:Accession: S02193
A:Molecule type: mRNA
A:Residues: 1-367 <SD>
A:Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
F:161,164,224,228/Binding site: zinc (Cys, His, Cys) #status predicted
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 23.0%; Score 778; DB 1; Length 367;
Best Local Similarity 44.1%; Pred. No. 5.8e-47;
Matches 164; Conservative 56; Mismatches 106; Indels 46; Gaps 7;
QY 15 FERLWSLEPDSYFDLPSSRGNNVYGGTSSMDVPHLEGMTTSVMAQFNLLSSTMQ 74
Db 15 FMDLWSMLPYSMOQLPLPDHSHWQEL-----SPLEP 46
QY 75 MSSRASASPYTPEHAASVPTHSPTAQSSFTDMSRAPVTPSNTDYPGPHHEVTFQOS 134
Db 47 SDPPPPPPPLPLAAPPPLNPPTPRA-----APSPVSTEDYGGDFRVGFVEA 101
QY 135 STAKSATWTSYLLAKLYCQIAKTCPIQIKYSTPTPPPGTATRAAMPVYKKAHVDVVKRC 194
Db 102 GTAKSVTCYSPVNLKVCRLAKPCVQVRGVGAPPDGSLSRAVAVYKKEHVAEVVRC 161
QY 195 PNEHGRDNEGQSPASHLIRVEGNNSQVDDPVTGRQSVVVPYPPQVGTFTILY 254
Db 162 PHHERCGGTG-D-LAPAOHLIRVEGNPOARYHDDTKRHSSVVVYPPPEVSGDCTVLY 220
QY 255 NFNCSNCGVGNRRPILIIILEMRDQVIGRSGFEGRICACPRDKADEHYREOQA 314
Db 221 NFNCSNCGVGNRRPILIIILEMRDQVIGRSGFEGRICACPRDKADEHYREOQA 314
QY 315 LNESSAKNGAAKRAFKGSPAPVAPGALGAGVKKRRHGDDETYLQVRGRENFEILMKLKS 374
Db 281 A-----GGVAKRA--MSPP-TEAPEPPKKRVLNPDNEIFYLQVRGRRRYEMKLKINEA 330
QY 375 LEIWE--LVPOP 384
Db 331 LQAEGGSAPRP 342

RESULT 3
S51648
cellular tumor antigen p53 - bovine
N:Alternate names: tumor-suppressor protein p53
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S51648
R:Dequiedt, F.; Willens, L.; Burny, A.; Kettmann, R.
submitted to the EMBL Data Library, September 1994
A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its g
A:Reference number: S51648
A:Accession: S51648
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-386 <DEQ>
A:Cross-references: EMBL:X81704; NID:g602333; PIDN:CAA57348.1; PID:g602333
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
F:168,171,231,235/Binding site: zinc (Cys, His, Cys) #status predicted
F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 22.5%; Score 760.5; DB 1; Length 386;
Best Local Similarity 44.2%; Pred. No. 1e-45;
Matches 169; Conservative 63; Mismatches 105; Indels 45; Gaps 11;
QY 60 SYMAQFNLLSSTMDQSSRAASAPYT-----PEHAASVPTHS-PPAQPSSFTDM 109
Db 24 NLLPENLLSS---ELSAVDLLPTVDATVDECPNEAPQPEPSAPAAPPAT---- 77
QY 110 SPAPV-----IPSNTPDYPGPHHEVTFQOSSTAKSATWTSYLLKLYCQIAKTCPI 161
Db 77 -PATATSWPLSSFFVPSOKTYPGNYGRFLQSGTAKSVTCYSPSLNKLFCQIAKTCPI 135
QY 162 QIKYSTPPPGTATRAAMPVYKKAHVDVVKRCNHELGRDFNEGQSPASHLIRVEGN 221
Db 136 QLWVDSPPPGTATRAAMPVYKKAHVDVVKRCNHELGRDFNEGQSPASHLIRVEGN 194
QY 222 LSQVDDPVTGRQSVVVPYPPQVGTFTILYNFNCSSCYGGMNRRPILIIILEMRD 281
Db 195 RAEYDDRNTFRHSVVVPIESPIDSECTIIHFNCSNCGVGNRRPILIIILEMRD 254
QY 282 GOVLGRSFEGRICACPRDKADEHYREQ-OALNNESSAKNGAAKRAFKGSPAPVAP 340
Db 255 GNLLGRNSFEVRCACPRDRRTTEENLRKKGSCPEPPR---STKRALPTNTSSPQ- 311
QY 341 GAGYKRRHGDDETYLQVRGRENFEILMKLKSLELMELVPOPLVDYSRQOQLLQRP 400
Db 311 ----PKKKPDGETFTLIQINGFKRYEMFRELNDALDKAL-----DGRPEGESRAHSS 360
QY 401 HLOP---PSYGPVLSPMNKVHG 419
Db 361 HLKSKRPSPSCHKKPKMKREG 382

RESULT 4
JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0633
R:Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992.
A:Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH0633; MUID:92210007
A:Accession: JH0633
A:Molecule type: mRNA
A:Residues: 1-396 <LEG>
A:Cross-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
A:Experimental source: kidney, strain MP1
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:179,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 22.1%; Score 749; DB 1; Length 396;
Best Local Similarity 43.8%; Pred. No. 6.8e-45;
Matches 165; Conservative 58; Mismatches 104; Indels 50; Gaps 10;
QY 14 TFEHLWSSLEPDSYFDLPQSSRGNNVYGGTSSMDVPHLEGMTTSVMAQFNLLSSTMD 73
Db 18 TFSDLKLLPPNNVLTLPSS-----DSIEELFLENVA-----GWLDPGE 59
QY 74 QMSRAASAPYTPPEHAASVP---THSPYAPQSSFTDMSAPV---IPSNTPDYPGPHH 127
Db 60 ALGSSAAAAPAP--AAEDPVAETPAPVASAPAT-----FWPLSSVPSYTKYGGDYGF 112
QY 128 EVTFQOSSTAKSATWTSYLLKLYCQIAKTCPIQIKYSTPTPPPGTATRAAMPVYKKAH 187
Db 113 RLGFLEHSGTAKSVTCYSPSLNKLFCQIAKTCPIVQVWVSSVTPPGTATRAAMPVYK 172

QY 188 TDVVKRCPNHELGRDNFEGOS-APASHLIRVEGNNLSOYVDDPVYTGROSVVVPYEPQVG 246
Db 173 TEVVRCPHRS-SEGDLAPQHLIRVEGNNHAEYLDKQTFRHSVVVPYEPPEVG 229
QY 247 TETTLINFMCSVGGNNRPILITLLEMDGOVLGRSFGRCACPGDRRADE 306
Db 230 SDCTTHYMCSSCGNNRPILITLLEDPGNNLGRNSFEVRCACPGDRRTEE 289
QY 307 DHREQ-QUALNESSAKNGAARAFKQSPAPVAPALGAGVKRRHDETYLVQVRGR 362
Db 290 KNFQKGEPCPELPPRSKRALPTNTSSSPQ-XXXXXXXXXXXXXKTKLDGEYFLKIRGQ 338
QY 363 ENFEILMKLESLEME 379
Db 339 ERFKQFQELNEALELKD 355

RESULT 5
JC6176
tumor suppressor protein p53 - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C:Accession: JC6176
R:Lee, H.; Larner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
A:Title: Cloning and Characterization of Chinese hamster p53 cDNA.
A:Reference number: JC6176; MUID:97183659
A:Contents: liver
A:Accession: JC6176
A:Molecule type: mRNA
A:Residues: 1-393 <LEE>
A:Cross-references: GB:U50395; NID:g1842229; PIDN:AA53040.1; PID:g1842230
C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage
ption, and recombination by protein/protein interactions.
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: liver; tumor

Query Match 21.98; Score 741.5; DB 2; Length 393;
Best Local Similarity 43.7%; Pred. No. 2.2e-44;
Matches 162; Conservative 57; Mismatches 111; Indels 41; Gaps 8;
QY 14 TFEHLWSLEPDSYFDLPQSSRGNNNEVGGTSDMDVPHLEGMTTSVMAQNLSSYMD 73
Db 18 TFSOLKLLPPNNVSLTSS-XXXXXXXXXXXXXDSIELFSENVTGWLSDSGALQGVAA 66
QY 74 QMSRAASAPYPEHAASVPTHSYAPQSPSTFTDMSAPVPSNTDYPGPHFFVTFQ 133
Db 67 AAATAEDPVETPAPVASAPA-TMPLSS-XXXXXXXXXXXXXVPSYKTFQDYGFRGLFH 115
QY 134 SSTAKSATWYSPLLKLYCOIAKTCPIQIKVSTPPPGCTATRAMPYVYKAEHVVDYKR 193
Db 116 SGTAHSVTCYFSLNKLFCQLAKTCVQLWVNSTPPGTRVRAAIYKKLYMTVEVRR 175
QY 194 CPNHELGRDNFEGOS-APASHLIRVEGNNLSOYVDDPVYTGROSVVVPYEPQVGFEFTTI 252
Db 176 CPHERS-SEGSLAPQHLIRVEGNNHAEYLDKQTFRHSVVVPYEPPEVSGDCTTI 232
QY 253 LYFMCNCSVGGNNRPILITLLEMDGOVLGRSFGRCACPGDRRADEHYREQ 312
Db 233 HYNMCNCSVGGNNRPILITLLEDPGNNLGRNSFEVRCACPGDRRTEKNFOK 292
QY 313 -QUALNESSAKNGAARAFKQSPAPVAPALGAGVKRRHDETYLVQVRGRNEFEIL 368
Db 293 GPCPELPPKSAKRALPTNTS-SSPP-XXXXXXXXXXXXXPKKLDGEYFLKIRGHRFAMF 341
QY 369 MKLESLEME 379
Db 342 QELNEALELKD 352

RESULT 6

A29376
cellular tumor antigen p53 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A29376; S61531; S72313; I51639
R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A:Title: Cloning and Characterization of a cDNA from Xenopus laevis coding for
A:Reference number: A29376; MUID:88143684
A:Accession: A29376
A:Molecule type: mRNA
A:Residues: 1-363 <SOU>
A:Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962
R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A:Title: Overexpression of wild-type p53 interferes with normal development in
A:Reference number: I51639; MUID:94134403
A:Accession: S61531
A:Molecule type: mRNA
A:Residues: 1-293, 295-363 <HOE>
A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.
submitted to the EMBL Data Library, March 1994
A:Reference number: S72313
A:Accession: S72313
A:Molecule type: mRNA
A:Residues: 1-51, 53-70, 72-293, 295-363 <HOW>
A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus
F:150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.9%; Score 741; DB 1; Length 363;
Best Local Similarity 41.7%; Pred. No. 2.2e-44;
Matches 169; Conservative 54; Mismatches 92; Indels 90; Gaps 12;
QY 1 MAQSTATSPD---GGTTFPHLWSSLEPD-XXXXXXXXXXXXXSTYFDLPQSSRGNNNEVGGT 45
Db 1 MEPSSETGMDPPLSQSTFTFDLWSSL-PDPQTQVTCRLDNLSEFPDYPLA-XXXXXXXXXXXX 49
QY 46 DSSMDYFHLEGMTTSVMAQNLSSSTMDQMSRAASAPYTPPEHAASVPTHSYAPQSPST 105
Db 49 -ADMTVLQ-EGLMGN-XXXXXXXXXXXXXAVPTVTS-XXXXXXXXXXXX 71
QY 106 FDTMSAPVPSNTDYPGPHFFVTFQSSSTAKSATWYSPLLKLYCOIAKTCPIQIKV 165
Db 71 -XXXXXXXXXXXXXVPSTDDYAGKYLQGLDFQNGTAKSVTCYSPELNKLFCQLAKTCPLLVV 121
QY 166 STPPPGTATRAMPYVYKAEHVVDYKRCNHELGRDNFEGOS-APASHLIRVEGNNLSQ 224
Db 122 ESPPPGSLTATAYKKEHVAEYVKKRCPHE--RSVEPGEDAAPSHLMRVEGNNLQAY 179
QY 225 YVDDPVYTGROSVVVPYEPQVGFEFTTLINFMCSVGGNNRPILITLLEMDGOV 284
Db 180 YMEDVNSGRHSVCVPEYEGVQGTCTTVLYNMCNCSVGGNNRPILITLLEMDGOV 239
QY 285 LGRRFEGFRICACPGDRRADEHYRQOQALNESSAKNGAARAFKQSPAPVAPALGAGV 344
Db 240 LGRRCFEYVACACPGDRRTEEDNYTKRGLKPS-XXXXXXXXXXXXXGRELAPSPSEPP-XXXX 289
QY 345 KRRR-XXXXXRGEDTYLVQVRGRNEFEILMKLESLEMEVPOPLV 386
Db 290 KRLVVVDDSEITLRIKGRSYEMIKKLNDALELQESLDQKV 334

RESULT 7
S02192

cellular tumor antigen p53 - rat
N/Alternate names: gene p53 protein; nuclear oncoprotein p53
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S02192; S41149
R/Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A/Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A/Reference number: S02192; MUID:89083585
A/Accession: S02192
A/Molecule type: mRNA
A/Residues: 1-391 <SOU>
A/Cross-references: EMBL:X13038; NID:g56828; PIDN:CAA31457.1; PID:g56829
R/Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A/Title: Structure of the rat p53 tumor suppressor gene.
A/Reference number: S41149; MUID:93181268
A/Accession: S41149
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-173; 'W', 175-391 <HUL>
A/Cross-references: EMBL:L07909
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C/Genetics:
A/Introns: 25/2; 32/3; 123/3; 185/1; 250/2; 305/1; 329/3; 365/2
C/Superfamily: cellular tumor antigen p53
C/Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
F:174,177,236,240/Binding site: zinc (Cys, His, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.7%; Score 735.5; DB 1; Length 391;
Best Local Similarity 42.8%; Pred. No. 5.8e-44;
Matches 167; Conservative 55; Mismatches 87; Indels 81; Gaps 12;
Db 14 TFEHLWSLEPDSYFDLPQSSRGNEVGGTDSMDVF-----HLEGTTSVMAQFN 66
Db 18 TFSCLWKLPPDDI---LPTTA-----TGSPNSMEDLPQDVAELLEG----- 59
Qy 67 LLSTMDQMSRAASAPYTPPEHAASVP-THSPYAPQSPSTFDTMSPAPV----- 115
Db 59 -----PEALQV--SAPAAQEPG---TEAPAPAPASATPWPPLSS 93
Qy 115 -IPSNTPDYPGPHFEVTFQSSAKSATWTYSPLKLYCQIAKTCPIQIKVSTPPPGT 173
Db 94 SVPSQKYQNGYFHLGSLGSAKSVMTCTYSLSLKLFCQIAKTCPVQLWYSTPPGT 153
Qy 174 AIRAMPYKKAHVTDVKKCPNHELGRDFNEGQSPASHLRVSGNLSQYVDDPVTVGR 233
Db 154 RVRAAIYKKSQHVTEVYRCPHERCSD-GDG-LAPPOHLIRVEGNPYAEYLDROTFR 211
Qy 234 QSVVVPYEPQVGTFTTILYNFMCNCSGCGNRRPILITILEMRDQGVILGRSFEGR 293
Db 212 HSVVVPYEPVSGDITTHYKNCSSCGMGNRRPILITILEMRDQGVILGRSFEGR 271
Qy 294 ICACPGDRKADHDHREQO-----ALNESAKNGAKRAFPQSPAPVAPALGAGVKRRH 349
Db 272 VCACPGDRTEENRKKKEHCPELPFGSA-----KRALPTSTSSSPQ-----QKKKP 320
Qy 350 GDETYVYLVQVRGRENFEILMKLESLEME 379
Db 321 LDGEYFLKIRGERFERFELNEALELKD 350

RESULT 8
JC6193
tumor suppressor p53 - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C/Accession: JC6193
R/Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.
Gene 185, 169-173, 1997
A/Title: cDNA cloning and immunological characterization of rabbit p53.

A/Reference number: JC6193; MUID:97208869
A/Accession: JC6193
A/Molecule type: mRNA
A/Residues: 1-391 <LEA>
A/Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:e194962; PID:g153
C/Genetics:
A/Genes: p53
C/Superfamily: cellular tumor antigen p53
C/Keywords: tumor

Query Match 21.4%; Score 724.5; DB 2; Length 391;
Best Local Similarity 43.5%; Pred. No. 3.4e-43;
Matches 165; Conservative 54; Mismatches 103; Indels 57; Gaps 10;
Db 21 STEP---DSTYFDLPQSSRGNEVGGTDSMDVFHLEGTTSVMAQFNLSSTMDQMS 77
Db 9 SLEPFLSQETFSDDLKLLPENL-----LTSNLPVVDLLSAED----- 49
Qy 78 RAASAPYTPPEHAASVP-THSPYAPQSPSTFDTMSPAPV-----IPSNTPDYPGPHFE 128
Db 49 -VANLNEDPEGLRVPAAPAPAPAPAPAPATSPWLSSSVPSQKTYHGNVGR 107
Qy 129 VTFQSSAKSATWTYSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHV 188
Db 108 LGLFSLGSAKSVMTCTYSPLKLYCQIAKTCPVQLWYDSTPPGTRVRAAIYKKSQHM 167
Qy 189 DVYKRCPNHELGRDFNEGQSPASHLRVSGNLSQYVDDPVTVGRQSVVYVYEPVPOVGT 248
Db 168 EVVRCPPHERCSD-SDG-LAPPOHLIRVEGNLRAEYLDROTFRHSVVPYEPVPGSD 225
Qy 249 FTILYNFMCNCSGCGNRRPILITILEMRDQGVILGRSFEGRICACPGDRKADHDH 308
Db 226 CTHIYNFMCNCSGCGMGNRRPILITILEMRDQGVILGRSFEGRVCAACPGDRRTTEEN 285
Qy 309 YEQCALNESAKNG-----AASKRAFPQSPAPVAPALGAGVKRRHDETYVLOVR 360
Db 286 FR-----KKEGECPELPQSSKRAL-----PTTTDSSPQTKKKPLDGEYFLKIR 331
Qy 361 GRENFEILMKLESLEME 379
Db 332 GREFERFERFELNEALELKD 350

RESULT 9
DNHJ3
cellular tumor antigen p53 - human
N/Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation supp
C/Species: Homo sapiens (man)
C/Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 23-Jun-1999
C/Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; B25397;
4805; I58354; I78850; I52681; S60153
R/Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986
A/Title: Characterization of the human p53 gene.
A/Reference number: A25224; MUID:87064416
A/Accession: A25224
A/Molecule type: DNA
A/Residues: 1-393 <LAW>
A/Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1;
R/Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
Gene 70, 245-252, 1988
A/Title: A variation in the structure of the protein-coding region of the human p53 g
A/Reference number: JT0436; MUID:89108008
A/Accession: A43073
A/Molecule type: DNA
A/Residues: 1-393 <BUC1>
A/Cross-references: EMBL:M22898; NID:g189474
A/Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro
A/Accession: JT0436
A/Molecule type: DNA
A/Residues: 1-71, 'P', 73-393 <BUC2>
A/Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476

A:Molecule type: mRNA
A:Residues: 1-393 <RIG>
A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho; predicted
F:176,179,236,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.2%; Score 718.5; DB 1; Length 393;
Best Local Similarity 42.1%; Pred.No.9e-43;
Matches 160; Conservative 58; Mismatches 103; Indels 59; Gaps 11;

QY 14 TFEHLSSLEPDSITYFDLPQSSRGNNVVGTTDSSNDVFHLEGMTTSVMAQFNLLSSTMD 73
DB 18 TFSDLWKLUPENVLSPLPSQA-----VDDL-----LSPDDLAQW-LTDDPGP 60
QY 74 QMSRAASASPYPTEHAASVPTHSYPAQSSFTDMSAP-----VIPSNTDYPGPHEF 127
DB 61 DEAPRUSERAP---HMAPTPAAPTAA-----APASWPLSSVPSOKTYHGSYGF 109
QY 128 EVTFQSSSTAKSATWTSYPLKLYLCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHV 187
DB 110 RLGLFHSGTAKSVCTYCTSPDLNKFQCOLAKTCVQLWVDSTPPPGSRVRAMAIYKOSQH 169
QY 188 TDVVKPCNHELGRDNEGOSAPASHLIRVEGNLSQYVDDPVTGRQSVVVPYEPQVGT 247
DB 170 TEVVRCPHERCD-SDG-LAPQHILRVEGNLRVYESSDRNTERHVSVPYEPPEVGS 227
QY 248 EFTTILYNFMCNCSVGGNNRRPILIIILEMRDGGVGLRRSFEGRICACPGDRKRAED 307
DB 228 DCTTIHYNMCNCSGMMNRRPILIIILEDSGMLLGNSEFVRVACPGDRRTEEE 287
QY 308 HYREQQALNESSAKG-----AASKRAFKOSPAVPALGAGVKKRRHGDEDTYVLQV 359
DB 288 NFR-----KKGEPCHELPFGSTKRALPNTSSSPQ-----PKKPLDGEYFTLQI 332
QY 360 RGRNFENFILMKLESLEME 379
DB 333 RGRERFEMPRELNEALEKD 352

RESULT 11
DNMS53
Cellular tumor antigen p53 - mouse
N:Alternate names: oncoprotein p53
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence revision 04-Oct-1996 #text change 22-Jun-1999
C:Accession: A22739; S06336; A02684; S38823; S38823; S40014; I48703
R:Blenz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A:Reference number: A22739; MUID:85027173
A:Accession: A22739
A:Molecule type: DNA
A:Residues: 1-134,'Y',136-390 <BIE>
A:Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;
R:Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
A:Reference number: S06336; MUID:88221682
A:Accession: S06336
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-134,'Y',136-390 <CHU>
R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Givol, D.
Nature 306, 594-597, 1983
A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
A:Reference number: A02684; MUID:84068204
A:Accession: A02684
A:Molecule type: mRNA
A:Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 <ZAK>
A:Cross-references: GB:X01237; GB:X01700; NID:g53575
R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640
A:Accession: S38822
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-390 <ARA1>
A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199
A:Accession: S38823
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167, 'G', '169-233', 'I', '235-390 <ARA2>
A:Cross-references: EMBL:M13873
R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
submitted to the EMBL Data Library, July 1988
A:Reference number: S40014
A:Accession: S40014
A:Molecule type: mRNA
A:Residues: 1-167, 'G', '169-390 <ARA3>
A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201
R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the p53 protein.
A:Reference number: I48703; MUID:84272240
A:Accession: I48703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-47, 'R', '49-78', 'OW', '82-390 <RES>
A:Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA5323.1; PID:g53571
C:Comment: This DNA-binding protein plays an essential role in the regulation of cell division. The tetramer association region may exhibit a beta-turn, beta-sheet, beta-tubule.
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:257-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7,9,12,18,23,37/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:173,176,235,239/Binding site: phosphate (Ser) (covalent) #status predicted
F:312/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
Query Match 21.0%; Score 711.5; DB 1; Length 390;
Best Local Similarity 43.2%; Pred. No. 2,7e-42;
Matches 159; Conservative 64; Mismatches 104; Indels 41; Gaps 12;
QY 14 TFEHLNLSLEPDSYFDLPQSSRGNNVGGTDSMDVFLHGMTSVMAQFNLLSSTD 73
DB 21 TFGSLWKLPPPE-----DILPSPHCMDLLLPQD--VEEF-FEGPSEAL----- 62
QY 74 QMSRAASASPY--TPEHAASVPHSPYAPQSPSTFTDMSAPVIPNDYDPPGPHFEVTF 131
DB 62 RVSGAPAAQDPVTETPGVPAPAPA--PLSSF-----VPSQTYQNGYGFHLGF 110
QY 132 QQSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPYKKAHVTDV 191
DB 111 LQSGTAKSVNCTYSPPLNKLFLQALAKTCVQLWVSATPPAGSRVRAMAIYKKSQHMTEV 170
QY 192 KRCPNHELGRDFNEGQAPASHLIRVEGNLSQYVDDPVTGQSVVVPYEPQVGEFTT 251
DB 171 RCPHERSCD-GDG-LAPQHLIRVEGNLYFEYLEDQTFHSHVVPYEPPEAGSYTT 228
QY 252 ILYNFCNCSVCGMNRRLIITLEMDGQVLGRSFEGRICACGCRDRKADEHYE 311

DB 229 IHTYMCNCSMGMMNRRLIITLEDDSSGNLGRDSFEYRVVCACPGDRRTTEENFRK 288
QY 312 QOALNESSAKNGAASAKRAKFPQPPAVPALGAGVKKKRRGHDEDTYVLOVGRGNEFEILMKL 371
DB 289 KEVLCPPLPGSA--KRALPTCTASAPP-----QKKKPLDGEYFTLKRGRKREMFREL 341
QY 372 KESLELME 379
DB 342 NEALELKD 349
RESULT 12
S38824
Cellular tumor antigen p53, minor splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38824; S35478
R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640
A:Accession: S38824
A:Molecule type: mRNA
A:Residues: 1-381 <ARA>
A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
R:Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A:Title: Alternatively spliced p53 RNA in transformed and normal cells of diffuse large B-cell lymphoma.
A:Reference number: S35478; MUID:92253421
A:Accession: S35478
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-381 <HANA>
A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
C:Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Comment: This sequence, produced by alternative splicing of the tenth intron, is not known.
C:Superfamily: cellular tumor antigen p53
C:Keywords: alternative splicing; phosphoprotein; zinc
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:267-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
Query Match 20.7%; Score 702; DB 2; Length 381;
Best Local Similarity 41.3%; Pred. No. 1.2e-41;
Matches 164; Conservative 69; Mismatches 114; Indels 50; Gaps 14;
QY 14 TFEHLNLSLEPDSYFDLPQSSRGNNVGGTDSMDVFLHGMTSVMAQFNLLSSTD 73
DB 21 TFGSLWKLPPPE-----DILPSPHCMDLLLPQD--VEEF-FEGPSEAL----- 62
QY 74 QMSRAASASPY--TPEHAASVPHSPYAPQSPSTFTDMSAPVIPNDYDPPGPHFEVTF 131
DB 62 RVSGAPAAQDPVTETPGVPAPAPA--PLSSF-----VPSQTYQNGYGFHLGF 110
QY 132 QQSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPYKKAHVTDV 191
DB 111 LQSGTAKSVNCTYSPPLNKLFLQALAKTCVQLWVSATPPAGSRVRAMAIYKKSQHMTEV 170
QY 192 KRCPNHELGRDFNEGQAPASHLIRVEGNLSQYVDDPVTGQSVVVPYEPQVGEFTT 251

```
Db 171 RRCPHHERCD-DGG-LAPQHLIRVEGNYLEYLEDQRTFRHSVYVYEPPEAGSEYTT 228
Qy 252 ILYNFMNCSSCVGMNRRPILITILEMRDGOVLGRSFEGRICACPGDRKADREHYRE 311
Db 229 IHXYMNCSSCMGMNRRPILITILEDSGGLGRDSFEVVCACPGDRRTTEENFRK 288
Qy 312 QOALNESSANKANGAKRAFQKSPAPVAGAGVKKRRGDEDTYYLYQVRGRENFEILMKL 371
Db 289 KEVLCPPEPPGSA--KRALPTCTASPP-----QKKPLDGEYFTLKIRGRKREMFREL 341
Qy 372 KESELMELVPLVDYSYRQOQLQRP-SHLQPPSY 407
Db 342 NEALELK-----DAHATESGDSRAHSSLOPRAF 370

RESULT 13
I46226
p53 - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46226
R:Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.
Anticancer Res. 14, 2039-2046, 1994
A:Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.
A:Reference number: I46226; MUID:95150524
A:Accession: I46226
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-77 <DEV>
A:Cross-references: GB:L27630; NID:g508454; PIDN:AAC37327.1; PID:g508455
C:Genetics:
A:Gene: p53
A:Introns: 24/1: 61/3
C:Superfamily: cellular tumor antigen p53

Query Match 7.3%; Score 248.5; DB 2; Length 77;
Best Local Similarity 61.5%; Pred. No. 5e-11;
Matches 48; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

Qy 183 KAEHYDVYKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQYVDDPVTGQSVVYVPEP 242
Db 1 KSEFVTEVYVRCPPHRCSDSDG-LAPPOHLIRVEGNLRAKYLDRTFRHSVYVYVPEP 59
Qy 243 POGTEFTTILYNFMNCNS 260
Db 60 PEVGFDTYTHNYMNCNS 77

RESULT 14
T00074
hypothetical protein KIAA0460 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 07-May-1999
C:Accession: T00074
R:Seiki, N.; Ohira, M.; Negase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A:Reference number: Z14085; MUID:98116662
A:Accession: T00074
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-903 <SEK>
A:Cross-references: EMBL:AB007929; NID:d1225338; PID:d1033327
C:Experimental source: brain
C:Genetics:
A:Note: KIAA0460

Query Match 4.5%; Score 151.5; DB 2; Length 903;
Best Local Similarity 21.1%; Pred. No. 0.0086;
Matches 175; Conservative 75; Mismatches 253; Indels 327; Gaps 45;
```

```
Qy 3 QSTATSPD-----GGTTFEHL-----WSSLEPDSYFDLPQSSRGNEVVGTD 46
Db 102 ESESTSPLEMKIHNFLKGNPGSGLNLPILSSLGSA-----PSESHPSDFQRGPTS 156
Qy 47 SMDVFLHEGM-----TTSVMAQFNLLSSTMDQMSRAASA-SP-- 85
Db 157 TSID--NIDGTPVDRSGTPTODMMDKPTSSSVDTMSLLSKIIISPGSSTPSSTRPPP 214
Qy 85 -----YYPEHAASVPTH-----SPYAOPTSTFTDMSAPVIPSNT----- 120
Db 215 GRDESYPRELSNSVYRPFGLSGSEPYKOPSGME--RPSSLMDSQKFKYDTSFQD 272
Qy 120 -----DYPGPHFEVTFQOSSTAKSA-----TWYSPLKLYCQIAKTCPIQIKV 165
Db 273 EDYRDFEYSGPPPSAMNLEKPAKSLKSLSDTXYQILSS-YSHRAQ--EFGVKS 329
Qy 166 STPPPGTAIRAMPVYKKAHVVDVVKRCP-----NHELGRD-----FN 204
Db 330 AFPP-----SVRAL-----LDSENCRLSSSGLFCGAFSVRGNEPGRSPSPSKN 376
Qy 205 EGOSAPASHLIRVEGNLS-----QYVDDP-----VTGROSVVYVY-EPP 243
Db 377 DSFTTPDSN-----HNSLSOSTTGLSLPKQKQYDPSHPVPHRSLSFSPQNTLAAPTGHPP 431
Qy 244 QVGTFTTILYNFMNCSSCVGMN-----RRPILIIILEMRDGOVLGRSFEGRIC-- 296
Db 432 TSGVE--KVLASTISTTIEFKNMLKNASRKP-----SDDKHFGQAPSKGTPSDG 480
Qy 296 -----ACPGDRKRAEDHYREQA-----LNESAKNGA-----ASKRAF 330
Db 481 VLSNLNQPSTATDQOQGEHYRIETRVSSCLDLPDSTEKGAPIETLGYHSASNRNM 540
Qy 331 KQSP-----PAVPALGAGVKRRHGEDT-----YYLQVRGRENFEILMKLESLEL----- 378
Db 541 SGEPIQTVESIRVPGKG--NRHGREASRVGWFDLSTSGSFDNGPSSASELASLGGGGS 598
Qy 378 -----MELVP--OPLVDYSYRQOQLQRP-SHLQ-----QVVGQPPPHSSAATNLGVPVGP 451
Db 599 GGLTGFTATYKERAQFQBSVGSFRSNTSTFEHLPPSLEHGTFFQRPVPGVPSAP 658
Qy 410 VLSPMKNVHGM-----NKLPSVN-----QVVGQPPPHSSAATNLGVPVGP 451
Db 659 PVPP--KDHGGITSDAPTHLPSVDLSNFTKEAALAHAAAPPPPGHSGSIFPPTPPP- 716
Qy 452 MLNNHGHAVPANGEMSSSHSAQSMVSGSCTPPPHYHADPSLVSP-----LTGLGCPNCIE 507
Db 716 -----PPPGHSS--SGSGGVFPSTPPPPPPVDSHGVVFPFAPPAEHHGVAGAVA 764
Qy 508 YFTSQGLQSIYH---LQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHDSYTAQQLRSS 564
Db 765 VFPKD-----HSSLQGLTAEHFGVLPGP-----RDHGGPTQ--RDL 799
Qy 565 NAATISGGSELQORVMEVHFVRHITIPN-----RGGPGGG 605
Db 800 NGPGLS-----RVRESLTLPSSHLEHLGPPHGGGGG 831

RESULT 15
T04518
hypothetical protein F16A16.80 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C:Accession: T04518
R:Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheisel, J.; M
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15376
A:Accession: T04518
A:Molecule type: DNA
A:Residues: 1-864 <BEV>
A:Cross-references: EMBL:AL035353
A:Experimental source: cultivar Columbia; BAC clone F16A16
C:Genetics:
```


A: Map position: 4
A: Note: Intron positions not resolved
A: Note: F16A16.80

```
Query Match      4.3%; Score 145; DB 2; Length 864;
Best Local Similarity 17.7%; Pred. No. 0.023;
Matches 100; Conservative 83; Mismatches 207; Indels 174; Gaps 22;

QY 95 THSPYAQPSTFTTMSAPVIP--SNTDY-----PQP 124
Db 91 TSTPATHQSSVSLPPPPPIAPYISGLDFGLGVKMMWNSYGKAAKFKASRHRDPFL 150
QY 125 HFEVTEQQSSTAKSATWYSPLLKLYCQ-IAKTCPIQKVS-----TPPPPGTAIRAM 178
Db 151 LPSAAAEVGEDEMASWLYHPLRQDYFSSGVASTSATPQSSASLAPTPPPSPVYGOI 210
QY 179 PVYKAEHVTDVVKRCPNHELGRDFNEG--QSAPASHLIRVEGNLSQYVDDPVTGROSV 236
Db 211 PVERRTENFNNFLRL-----RGNIFSGRVEAGP---VVIESTQIGSSATPSSAAESC 261
QY 237 VVYEPPOVGTETTYLYNPMCNSSCVGGNNRAPILIIITLEMRDGOVLGRR-----SFEQ 292
Db 262 VI---PATHTESRAAATGVSTFAVPGLGRR-----GKEYATETAGTSYSG 306
QY 293 -----RICACPRDRKKADEHYREQ--QALNESSAKNGAAKRAFKQSPPAVPALGAG 343
Db 307 VNKAETERVQIQPERTKITEDKKRETTAEIQGTAEAGSTSR----- 351
QY 344 VKRRRGDEDT-----YLVQVRG-----NFEILMKLAKES 374
Db 351 -KRSRAADHNLSEVLITFYLETGKQDREDENSARTSPSLQKDSNKGFKVSWKINAN 409
QY 375 L--ELMELVPOPLVDSYRQQQLQRPShLPP-----SYGPVLSPMKNVHGKMKL 424
Db 410 LISHVLELITEILVIESMLLCQMSMGHGMPPMHGEGNTQQFNPMHMGWK---GMNRP 466
QY 425 PSYNQLVGOPPPHSSAATNLGPGVGMNLNHHGAVPA-----NGEMSSSHSAQSNVSGSH 480
Db 467 PPEVPPPGKTFPR-----PGHMAGVGPSPYALRYPPFPDPTQASDLRSRVHPSLH 514
QY 481 CTPPPPYHADPSLVSELTGLGCPNCEIYFTSGLQSIYHLQNLITIEDLGALKIPEQYMT 540
Db 515 SNVPNQPRPAYIN-----PYSQFVGLHMQ-----QPPLPLQVI 550
QY 541 INWGLQDLKQGHDYSTAQQLRSS 564
Db 551 LSOYLLPVNQHHSLVSATQVLASN 574
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Search completed: April 25, 2000, 20:19:02
Job time: 4490 sec